

SEQUENCE LISTING

<110> Cytos Biotechnology AG

<120> Polypeptides involved in cell-entry of the Adenoviruses of Subtype B

<130> C62115EP

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<170> PatentIn version 3.1

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Lys Pro Lys Pro Tyr Tyr Glu Glu Arg Val Asp Tyr Lys Cys

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55

60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
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the STP-B region of CD46 in certain splice variants of CD46

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ccaaagtgtc taaaagggtcc taggcctact tacaagcctc cagtcctaaa ttatccagga	900
tatcctaaac ctgaggaagg aatacttgac agtttggatg tt	942

- 13 -

<210> 13

<211> 314

<212> PRT

<213> homo sapiens

<400> 13

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

- 14 -

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
 210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
 225 230 235 240

Gly Phe Gly Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
 245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
 260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Gly Pro Arg
 275 280 285

Pro Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro
 290 295 300

Glu Glu Gly Ile Leu Asp Ser Leu Asp Val
 305 310

<210> 14

<211> 945

<212> DNA

<213> homo sapiens

<400> 14	
atggagcctc ccggccgccc cgagtgtccc ttcccttccc ggccctttcc tgggttgctt	60
ctggcgccca tggtgttgct gctgtactcc ttctccgatg cctgtgagga gccaccaaca	120
tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta	180
gattataagt gtaaaaaagg atacttctat ataccccttc ttgccaccca tactatttgt	240
gatcggaaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca	300
tatatacggg atcctttaaa tggccaagca gtccctgcaa atgggactta cgagtttggt	360
tatcagatgc actttatggtaatgagggt tattacttaa ttggtaaga aattctatat	420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc ccccaatatg tgaaaagggtt	480
ttgtgtacac cacctccaaa aataaaaaat ggagaacaca ccttttagtga agtagaagta	540
ttttagtatac ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt	600
tcacttatttgg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct	660

- 15 -

ccagagtgtta aagtggcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca	720
ggattttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggttt	780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttgga tccccagtt	840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca	900
ggatatccta aacctgagga aggaatactt gacagttgg atgtt	945

<210> 15

<211> 315

<212> PRT

<213> homo sapiens

<400> 15

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe			
1	5	10	15
10	15		

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser			
20	25	30	
30			

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly			
35	40	45	
45			

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys			
50	55	60	
60			

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys			
65	70	75	80
75	80		

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg			
85	90	95	
95			

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro			
100	105	110	
110			

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn			
115	120	125	
125			

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys			
130	135	140	
140			

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val			
145	150	155	160
155	160		

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Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Glu His Thr Phe Ser
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
 180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Tyr Pro Lys
290 295 300

Pro Glu Glu Gly Ile Leu Asp Ser Leu Asp Val
305 310 315

<210> 16

<211> 987

<212> DNA

<213> homo sapiens

<400> 16

atggagccctc ccggccggcg cgagtgtccc tttcccttctt ggccgctttcc tgggttgtttt 60

ctggcgccca tgggtttgttgc gctgtactcc ttctccgatg cctgtgagga gccaccaaca 120

tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tqaacqagta 180

gattataaqt gtaaaaaaaagg atacttctat ataccccttc ttggccaccca tactatttgt 240

gatcgaaatc atacatggct acctgtctca gatgacgcct gttataagaga aacatgtcca 300

tatataaaaa atccccccca tggggaaaggc atccactccaa atggggatttt ccgtttttat 362

- 17 -

tatcagatgc actttatttg taatgagggt tattacttaa ttggtaaga aattctatat	420
tgtgaactta aaggatca gtcaattgg agcgtaagc ccccaatatg tgaaaaggtt	480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta	540
tttgagtatc ttgatgcagt aacttatagt tgtatcctg cacctggacc agatccattt	600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct	660
ccagagtgtaa aagtggtaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca	720
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt	780
tacccgtatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tcccccaagtt	840
ccaaagtgtc taaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca	900
ggtccttaggc ctacttacaa gcctccagtc tcaaattatc caggatatcc taaaacctgag	960
gaaggaatac ttgacagttt ggatgtt	987

<210> 17

<211> 329

<212> PRT

<213> homo sapiens

<400> 17

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe	
1	5
10	15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser	
20	25
30	

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly	
35	40
45	

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys	
50	55
60	

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys	
65	70
75	80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg	
85	90
95	

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro	
100	105
110	

- 18 -

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
145 150 155 160

Leu Cys Thr Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
225 230 235 240

Gly Phe Gly Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro
290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val
325

<210> 18

<211> 1671

<212> DNA

- 19 -

<213> artificial sequence

<220>

<223> Construct encoding a fusion polypeptide between the extracellular domain of CD46 at the N-terminus and a human Fc-gamma3 domain at the C-terminus

<400> 18

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ctggcggcca	tggtgttgct	gctgtactcc	ttctccgatg	cctgtgagga	gccaccaaca	120
tttgaagcta	tggagctcat	tggtaaacca	aaaccctact	atgagattgg	tgaacgagta	180
gattataagt	gtaaaaaaagg	atacttctat	atacccctcc	ttgccaccca	tactatttgt	240
gatecggaatc	atacatggct	acctgtctca	gatgacgcct	gttatagaga	aacatgtcca	300
tatatacggg	atcctttaaa	tggccaagca	gtccctgcaa	atgggactta	cgagtttggt	360
tatcagatgc	acttttatttgc	taatgagggt	tattacttaa	ttggtaaga	aattctatata	420
tgtgaactta	aaggatcagt	agcaatttgg	agcggtaaagc	ccccaaatatg	tgaaaaggtt	480
tttgttacac	cacccctaaaa	aataaaaaat	ggaaaacaca	ccttttagtga	agtagaaagta	540
ttttagtatac	ttttagtgcagt	aacttatagt	tgtgatcctg	cacccggacc	agatccattt	600
tcacttatttgc	gagagagcac	gattttattgt	ggtgacaattt	cagtgtggag	tctgtctgt	660
ccagagtgtt	aagtggtcaa	atgtcgattt	ccagtagtcg	aaaatggaaa	acagatatca	720
ggattttggaa	aaaaatttta	ctacaaagca	acagttatgt	ttgaatgcga	taagggtttt	780
taccccgatg	gcagcgacac	aattgtctgt	gacagtaaca	gtacttggga	tccccccagtt	840
ccaaagtgtc	ttaaagtgtc	gacttcttcc	actacaaaat	ctccagcgtc	cagtgcctca	900
ggtccttaggc	ctacttacaa	gcctccagtc	tcaaatttac	caggatatcc	taaacctgag	960
gaaggaatac	ttgacagttt	ggatgttaag	cttactcaca	catgcccacc	gtgcccagca	1020
cctgaagccg	agggggcacc	gtcagtccttc	ctcttcccccc	caaaacccaa	ggacaccctc	1080
atgatctccc	ggacccttga	ggtcacatgc	gtgggtgggg	acgtgagcca	cgaagaccct	1140
gaggtcaagt	tcaactggta	cgtggacggc	gtggaggtgc	ataatgcca	gacaaaggccg	1200
cgggaggagc	agtacaacag	cacgtaccgt	gtggtcagcg	tcctcaccgt	cctgcaccag	1260
gactggctga	atggcaagga	gtacaagtgc	aaggcttcca	acaaagccct	cccagcctcc	1320
atcgagaaaa	ccatctccaa	agccaaaggg	cagccccgag	aaccacaggt	gtacaccctg	1380
cccccatccc	ggatgagct	gaccaagaac	caggtcagcc	tgacccctgc	ggtcaaaggc	1440
ttctatcccc	gcgacatcgc	cgtggagtg	gagagcaatg	ggcagccgga	gaacaactac	1500
aagaccacgc	ctcccggtt	ggactccgac	ggctccctct	tcctctacag	caagctcacc	1560

- 20 -

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gtcgggtat gcatgaggct 1620
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaatg a 1671

<210> 19

<211> 556

<212> PRT

<213> artificial sequence

<220>

<223> fusion polypeptide between the extracellular domain of CD46 at the N-terminus and a human Fc-gamma3 domain at the C-terminus

<400> 19

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Ile Leu Tyr Cys Glu Leu Lys
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
145 150 155 160

Leu Cys Thr Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser

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165

170

175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
225 230 235 240

Gly Phe Gly Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro
290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val Lys Leu Thr His Thr Cys Pro
325 330 335

Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
340 345 350

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
355 360 365

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
370 375 380

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
385 390 395 400

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
405 410 415

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Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 420 425 430

Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala
 435 440 445

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 450 455 460

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 465 470 475 480

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 485 490 495

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 500 505 510

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 515 520 525

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 530 535 540

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 545 550 555

<210> 20

<211> 1746

<212> DNA

<213> artificial sequence

<220>

<223> Construct encoding a fusion polypeptide between the extracellular domain of CD46 at the N-terminus and the scFv FRP5 against ErbB-2 at the C-terminus

<400> 20
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 ctggcgccca tgggtttgct gctgtactcc ttctccgatg cctgtgagga gccaccaaca 120
 tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta 180
 gattataagt gtaaaaaaagg atacttctat atacctcctc ttgccaccca tactatttgt 240
 gatcggaaatc atacatggct acctgtctca gatgacgctt gttatagaga aacatgtcca 300

- 23 -

tatatacggg atcctttaaa tgcccaagca gtcctgcaa atggactta cgagttttgt	360
tatcagatgc actttatgg taatgagggt tattacttaa ttggtaaga aattctatat	420
tgtgaactta aaggatcagt agcaattgg agcggttaagc ccccaatatg tgaaaaggtt	480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca ccttagtga agtagaagta	540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt	600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtggtgg tcgtgctgct	660
ccagagtgtaa aagtggtaaa atgtcgattt ccagtagtgc aaaatggaaa acagatata	720
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt	780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tcccccaagtt	840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgccctca	900
ggtccttaggc ctacttacaa gcctccagtc tcaaattatc caggatatcc taaacctgag	960
gaaggaatac ttgacagttt ggatgttggc ggccgccttc aggtacaact gcagcagtct	1020
ggacctgaac tgaagaagcc tggagagaca gtcaagatct cctgcaaggc ctctggtat	1080
ccttcacaa actatggaaat gaactgggtg aagcaggctc caggacaggg tttaaagtgg	1140
atgggctgga ttaacacttc cactggagag tcaacatttgc ctgatgactt caaggacgg	1200
tttgacttctt ctttggaaac ctctgccaac actgcctatt tgcatatcaa caacctcaa	1260
agtgaagaca tggctacata tttctgtgca agatgggagg tttaccacgg ctacgttcc	1320
tactggggcc aagggaccac ggtcaccgtt tcctctggcg gtggcggttc tgggtggcggt	1380
ggctccggcg gtggcggttc tgacatccag ctgaccagt ctcacaaatt cctgtcoact	1440
tca tagtggag acagggtcag catcacctgc aaggccagtc aggtatgtta taatgctgtt	1500
gcctggtatac aacagaaacc aggacaatct cctaaacttc tgatattactc ggcacatctcc	1560
cgg tacactg gagtccttc tcgcttact ggcagtggtt ctggggccgga tttcaatttc	1620
accatcagca gtgtcaggc tgaagacatcg gcagtttatt tctgtcagca acattttcgt	1680
actccattca cgttcggctc ggggacaaaa ttggagatcg actacaagga tgacgacgac	1740
aagtag	1746

<210> 21

<211> 581

<212> PRT

<213> artificial sequence

- 24 -

<220>

<223> fusion polypeptide between the extracellular domain of CD46 at the N-terminus and the scFv FRP5 against ErbB-2 at the C-terminus

<400> 21

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
210 215 220

- 25 -

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro
290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val Gly Gly Arg Ser Gln Val Gln
325 330 335

Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Lys
340 345 350

Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn
355 360 365

Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile
370 375 380

Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe Lys Gly Arg
385 390 395 400

Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile
405 410 415

Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys Ala Arg Trp
420 425 430

Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly Thr Thr Val
435 440 445

Thr Val Ser Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe Leu Ser Thr
465 470 475 480

- 26 -

Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val
485 490 495

Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
500 505 510

Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val Pro Ser Arg
515 520 525

Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr Ile Ser Ser
530 535 540

Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Phe Arg
545 550 555 560

Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys
580